

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/042,583

OIPE 0300

#5

DATE: 03/31/98  
TIME: 13:54:18

INPUT SET: S24576.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Ni, Jian  
Gentz, Reiner  
Yu, Guo-Liang  
Su, Jeffrey  
Rosen, Craig A.

(ii) TITLE OF INVENTION: Death Domain Containing Receptor 5

(iii) NUMBER OF SEQUENCES: 12

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.  
(B) STREET: 9410 Key West Avenue  
(C) CITY: Rockville  
(D) STATE: MD  
(E) COUNTRY: US  
(F) ZIP: 20850

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US herewith  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/054,021  
(B) FILING DATE: 29-JUL-1997

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/040,846  
(B) FILING DATE: 17-MAR-1997

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hoover, Kenley  
(B) REGISTRATION NUMBER: 40,302  
(C) REFERENCE/DOCKET NUMBER: PF366

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/042,583DATE: 03/31/98  
TIME: 13:54:20

INPUT SET: S24576.raw

47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: 3013098504  
49 (B) TELEFAX: 3013098439  
50  
51  
52 (2) INFORMATION FOR SEQ ID NO:1:  
53  
54 (i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 1600 base pairs  
56 (B) TYPE: nucleic acid  
57 (C) STRANDEDNESS: single  
58 (D) TOPOLOGY: linear  
59  
60 (ii) MOLECULE TYPE: DNA (genomic)  
61  
62  
63 (ix) FEATURE:  
64 (A) NAME/KEY: sig\_peptide  
65 (B) LOCATION: 130..283  
66  
67 (ix) FEATURE:  
68 (A) NAME/KEY: CDS  
69 (B) LOCATION: 130..1362  
70  
71 (ix) FEATURE:  
72 (A) NAME/KEY: mat\_peptide  
73 (B) LOCATION: 284..1362  
74  
75  
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
77  
78 CACGCGTCCG CGGGCGCGGC CGGAGAACCC CGCAATCTTT GCGCCACAAA AATACACCGA 60  
79  
80 CGATGCCCCGA TCTACTTTAA GGGCTGAAAC CCACGGGCCT GAGAGACTAT AAGAGCGTTC 120  
81  
82 CCTACCGCC ATG GAA CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG 168  
83 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly  
84 -51 -50 -45 -40  
85  
86 GCC CGG AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC AGG 216  
87 Ala Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg  
88 -35 -30 -25  
89  
90 CCT GGG CCC CGG GTC CCC AAG ACC CTT GTG CTC GTT GTC GCC GCG GTC 264  
91 Pro Gly Pro Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val  
92 -20 -15 -10  
93  
94 CTG CTG TTG GTC TCA GCT GAG TCT GCT CTG ATC ACC CAA CAA GAC CTA 312  
95 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu  
96 -5 1 5 10  
97  
98 GCT CCC CAG CAG AGA GCG GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA 360  
99 Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/042,583

DATE: 03/31/98  
TIME: 13:54:21

INPUT SET: S24576.raw

	15	20	25	
100				
101				
102	GAG GGA TTG TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT			408
103	Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp			
104	30	35	40	
105				
106	TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC TGG AAT GAC			456
107	Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp			
108	45	50	55	
109				
110	CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT GAT TCA GGT GAA GTG GAG			504
111	Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu			
112	60	65	70	
113				
114	CTA AGT CCC TGC ACC ACG ACC AGA AAC ACA GTG TGT CAG TGC GAA GAA			552
115	Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu			
116	75	80	85	90
117				
118	GGC ACC TTC CGG GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC			600
119	Gly Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg			
120	95	100	105	
121				
122	ACA GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA CCC TGG			648
123	Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp			
124	110	115	120	
125				
126	AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC ATC ATC ATA GGA GTC			696
127	Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val			
128	125	130	135	
129				
130	ACA GTT GCA GCC GTA GTC TTG ATT GTG GCT GTG TTT GTT TGC AAG TCT			744
131	Thr Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser			
132	140	145	150	
133				
134	TTA CTG TGG AAG AAA GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT			792
135	Leu Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly			
136	155	160	165	170
137				
138	GGT GGT GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT GGG			840
139	Gly Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly			
140	175	180	185	
141				
142	GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC TTG CAG CCC ACC			888
143	Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr			
144	190	195	200	
145				
146	CAG GTC CCT GAG CAG GAA ATG GAA GTC CAG GAG CCA GCA GAG CCA ACA			936
147	Gln Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr			
148	205	210	215	
149				
150	GGT GTC AAC ATG TTG TCC CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG			984
151	Gly Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro			
152	220	225	230	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/042,583

DATE: 03/31/98  
TIME: 13:54:23

INPUT SET: S24576.raw

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153
154   GCA GAA GCT GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT      1032
155   Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
156   235                               240                               245                               250
157
158   GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT GAC TTT GCA      1080
159   Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala
160                               255                               260                               265
161
162   GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG CTC ATG AGG AAG TTG GGC      1128
163   Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly
164                               270                               275                               280
165
166   CTC ATG GAC AAT GAG ATA AAG GTG GCT AAA GCT GAG GCA GCG GGC CAC      1176
167   Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His
168                               285                               290                               295
169
170   AGG GAC ACC TTG TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG      1224
171   Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly
172   300                               305                               310
173
174   CGA GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG CTG GGA      1272
175   Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly
176   315                               320                               325                               330
177
178   GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC TTG TTG AGC TCT GGA      1320
179   Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly
180                               335                               340                               345
181
182   AAG TTC ATG TAT CTA GAA GGT AAT GCA GAC TCT GCC ATG TCC      1362
183   Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
184                               350                               355                               360
185
186   TAAGTGTGAT TCTCTTCAGG AAGTGAGACC TTCCCTGGTT TACCTTTTTT CTGGAAAAAG      1422
187
188   CCCAACTGGA CTCCAGTCAG TAGGAAAGTG CCACAATTGT CACATGACCG GTACTGGAAG      1482
189
190   AAACCTCTCCC ATCCAACATC ACCCAGTGGA TGGAACATCC TGTAACCTTTT CACTGCACCT      1542
191
192   GGCATTATTT TTATAAGCTG AATGTGATAA TAAGGACACT ATGGAAAAAA AAAAAAAA      1600
193
194
195   (2) INFORMATION FOR SEQ ID NO:2:
196
197       (i) SEQUENCE CHARACTERISTICS:
198           (A) LENGTH: 411 amino acids
199           (B) TYPE: amino acid
200           (D) TOPOLOGY: linear
201
202       (ii) MOLECULE TYPE: protein
203
204       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
205

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/042,583

DATE: 03/31/98  
TIME: 13:54:25

INPUT SET: S24576.raw

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206 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
207 -51 -50 -45 -40
208
209 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
210 -35 -30 -25 -20
211
212 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
213 -15 -10 -5
214
215 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
216 1 5 10
217
218 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
219 15 20 25
220
221 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
222 30 35 40 45
223
224 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
225 50 55 60
226
227 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
228 65 70 75
229
230 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
231 80 85 90
232
233 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
234 95 100 105
235
236 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
237 110 115 120 125
238
239 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
240 130 135 140
241
242 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
243 145 150 155
244
245 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
246 160 165 170
247
248 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
249 175 180 185
250
251 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
252 190 195 200 205
253
254 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
255 210 215 220
256
257 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
258 225 230 235

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PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/042,583**

DATE: 03/31/98  
TIME: 13:54:27

*INPUT SET: S24576.raw*

Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: US herewith